

SEQUENCE LISTING

<110> HARA, SEIICHI
YOKOZEKI, KENZO
ABE, ISAO
TONOUCHI, NAOTO
JOJIMA, YASUKO

<120> NOVEL PEPTIDE-FORMING ENZYME GENES

<130> 247848US0

<150> JP 2003-16765
<151> 2003-01-24

<150> US 60/491,612
<151> 2003-08-01

<160> 27

<170> PatentIn version 3.1

<210> 1
<211> 9
<212> PRT
<213> Empedobacter brevis

<400> 1

Leu Phe Thr Ala Ile Tyr Gln Pro Lys
1 5

<210> 2
<211> 9
<212> PRT
<213> Empedobacter brevis

<400> 2

Thr Asn Val Thr Tyr Thr Met Pro Asp
1 5

<210> 3
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<220>
<221> misc_feature

<222> (6)..(6)
<223> n = a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(9)
<223> n = a, c, g, or t

<400> 3
ttyacngcna thtaycarcc

20

<210> 4
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic DNA

<220>
<221> misc_feature
<222> (3)..(3)
<223> n = a, c, g, or t

<220>
<221> misc_feature
<222> (9)..(9)
<223> n = a, c, g, or t

<220>
<221> misc_feature
<222> (15)..(15)
<223> n = a, c, g, or t

<220>
<221> misc_feature
<222> (18)..(18)
<223> n = a, c, g, or t

<400> 4
tcnggcatng trtangtnac rtt

23

<210> 5
<211> 2024

<213> Empedobacter brevis

<223>

tcg tat cct ggt ttt tat tcg aca atg agt ttg gtt aat tcg cat cca 588

Ser	Tyr	Pro	Gly	Phe 165	Tyr	Ser	Thr	Met	Ser 170	Leu	Val	Asn	Ser	His 175	Pro	
act	cta	aaa	gcc	ggt	tcg	cca	caa	gcg	ccc	ggt	acc	aat	tgg	ttt	tta	636
Thr	Leu	Lys	Ala 180	Val	Ser	Pro	Gln	Ala 185	Pro	Val	Thr	Asn	Trp 190	Phe	Leu	
ggt	gac	gat	ttt	cat	cat	aat	gga	ggt	tta	ttc	ttg	aat	gat	tct	ttc	684
Gly	Asp	Asp 195	Phe	His	His	Asn	Gly 200	Val	Leu	Phe	Leu	Asn 205	Asp	Ser	Phe	
tca	ttt	atg	act	ttt	ttt	ggt	gta	aaa	cgt	ccg	caa	cca	att	acg	cca	732
Ser	Phe 210	Met	Thr	Phe	Phe	Gly 215	Val	Lys	Arg	Pro	Gln 220	Pro	Ile	Thr	Pro	
gat	aaa	ggt	ccg	aaa	cgt	ttt	gaa	tat	cca	ata	aaa	gat	aat	tat	aga	780
Asp 225	Lys	Gly	Pro	Lys	Arg 230	Phe	Glu	Tyr	Pro	Ile 235	Lys	Asp	Asn	Tyr	Arg 240	
ttt	tat	gca	agt	ggc	tct	gta	aaa	gag	ttg	aaa	gat	aaa	tat	ttg	caa	828
Phe	Tyr	Ala	Ser	Gly 245	Ser	Val	Lys	Glu	Leu 250	Lys	Asp	Lys	Tyr	Leu 255	Gln	
gat	aat	atc	aag	ttt	tac	aat	gat	tta	ttt	gcg	cat	cca	gat	tac	gat	876
Asp	Asn	Ile	Lys 260	Phe	Tyr	Asn	Asp	Leu 265	Phe	Ala	His	Pro	Asp 270	Tyr	Asp	
caa	ttt	tgg	caa	gat	cgt	aat	ggt	tta	cca	cat	tta	act	aac	gtg	caa	924
Gln	Phe	Trp 275	Gln	Asp	Arg	Asn	Val 280	Leu	Pro	His	Leu	Thr 285	Asn	Val	Gln	
cct	gct	gta	atg	acg	ggt	gga	ggt	ttt	ttt	gat	gca	gaa	gat	gtc	tac	972
Pro	Ala 290	Val	Met	Thr	Val	Gly 295	Gly	Phe	Phe	Asp	Ala 300	Glu	Asp	Val	Tyr	
ggc	gct	ttc	gaa	acg	tat	aaa	gca	att	gag	aaa	caa	aat	ccg	aaa	gca	1020
Gly 305	Ala	Phe	Glu	Thr	Tyr 310	Lys	Ala	Ile	Glu	Lys 315	Gln	Asn	Pro	Lys	Ala 320	
aca	aat	att	atg	ggt	gcc	gga	cct	tgg	ttt	cat	ggt	ggt	tgg	ggt	cgt	1068
Thr	Asn	Ile	Met	Val 325	Ala	Gly	Pro	Trp	Phe 330	His	Gly	Gly	Trp 335	Val	Arg	
agc	aac	gga	agt	act	ttt	gga	gat	atg	caa	ttt	gca	tcg	aat	aca	agt	1116
Ser	Asn	Gly	Ser 340	Thr	Phe	Gly	Asp	Met 345	Gln	Phe	Ala	Ser	Asn 350	Thr	Ser	
gag	cat	tat	cag	caa	gaa	ata	gaa	ttg	cct	ttt	ttt	aat	tat	tac	tta	1164
Glu	His	Tyr 355	Gln	Gln	Glu	Ile	Glu 360	Leu	Pro	Phe	Phe	Asn 365	Tyr	Tyr	Leu	
aaa	gat	aaa	ggt	aat	ttt	aaa	cca	acc	gaa	gct	aca	att	ttt	att	acg	1212

Lys 370	Asp	Lys	Gly	Asn	Phe	Lys 375	Pro	Thr	Glu	Ala	Thr 380	Ile	Phe	Ile	Thr	
gga 385	tct Ser	aac Asn	gaa Glu	tgg Trp	aaa Lys 390	caa Gln	ttt Phe	gat Asp	gct Ala	tgg Trp 395	cca Pro	cca Pro	aaa Lys	aat Asn	gta Val 400	1260
aca Thr	aca Thr	caa Gln	aaa Lys	att Ile 405	tat Tyr	ttg Leu	caa Gln	caa Gln	aat Asn 410	ggt Gly	aaa Lys	ata Ile	gct Ala	ttt Phe 415	aat Asn	1308
aaa Lys	acc Thr	aat Asn	aca Thr 420	aca Thr	act Thr	act Thr	ttt Phe	gac Asp 425	gaa Glu	tat Tyr	ggt Val	gca Ala	gat Asp 430	cca Pro	aat Asn	1356
tct Ser	cca Pro	gtt Val 435	cct Pro	tat Tyr	tca Ser	gga Gly	gga Gly 440	gtt Val	tta Leu	gaa Glu	act Thr	cgt Arg 445	tca Ser	aga Arg	gaa Glu	1404
tat Tyr 450	atg Met	gtc Val	gat Asp	gat Asp	caa Gln	cgc Arg 455	ttt Phe	gct Ala	tct Ser	act Thr	cgt Arg 460	cct Pro	gat Asp	gtt Val	atg Met	1452
gtg Val 465	tat Tyr	caa Gln	tct Ser	gat Asp	att Ile 470	ttg Leu	aca Thr	gaa Glu	gat Asp	att Ile 475	acg Thr	ctt Leu	gct Ala	ggt Gly	cct Pro 480	1500
gtt Val	atc Ile	aat Asn	cat His 485	tta Leu	gtg Val	gtt Val	tct Ser	act Thr	acg Thr 490	gga Gly	aca Thr	gac Asp	gct Ala	gat Asp 495	tat Tyr	1548
gtt Val	gta Val	aaa Lys	ttg Leu 500	att Ile	gat Asp	gtt Val	tat Tyr	cct Pro 505	gaa Glu	aac Asn	acg Thr	cca Pro	aaa Lys 510	ttt Phe	aat Asn	1596
aac Asn	aaa Lys	tta Leu 515	atg Met	gct Ala	gga Gly	tat Tyr	caa Gln 520	aat Asn	ttg Leu	att Ile	cgt Arg	gca Ala 525	gaa Glu	att Ile	atg Met	1644
cgc Arg 530	gga Gly	aaa Lys	tat Tyr	aga Arg	aat Asn	agt Ser 535	ttc Phe	tct Ser	aac Asn	ccc Pro	gaa Glu 540	gct Ala	atg Met	gtt Val	ccg Pro	1692
aat Asn 545	aaa Lys	gaa Glu	aca Thr	aat Asn	gta Val 550	acg Thr	tac Tyr	acg Thr	atg Met	cca Pro 555	gat Asp	gtt Val	gga Gly	cat His	aca Thr 560	1740
ttt Phe	aag Lys	aaa Lys	gga Gly	cat His 565	cgc Arg	att Ile	atg Met	att Ile	caa Gln 570	gtt Val	cag Gln	aac Asn	agt Ser	tgg Trp 575	ttt Phe	1788
cct	tta	gca	gat	cgc	aat	ccg	caa	caa	ttt	atg	aat	gtt	tac	gaa	gca	1836

Pro Leu Ala Asp Arg Asn Pro Gln Gln Phe Met Asn Val Tyr Glu Ala
580 585 590

act tct aaa gat tat tta aaa caa acg caa cga att tat cat act tct 1884
Thr Ser Lys Asp Tyr Leu Lys Gln Thr Gln Arg Ile Tyr His Thr Ser
595 600 605

tat atc gaa att ccg gta ttg aaa taacaaaaaa atccagctaa ttagctggat 1938
Tyr Ile Glu Ile Pro Val Leu Lys -
610 615

tttttttata atgttacttt tcctattttt cctttatttc caactaaaat tacatatttt 1998

ttatcgggcg aaaccgtaca agtatg 2024

<210> 6
<211> 616
<212> PRT
<213> Empedobacter brevis

<400> 6

Val Lys Lys Leu Thr Leu Lys Val Thr Leu Leu Thr Leu Leu Leu Gly
1 5 10 15

Ser Thr Val Gly Phe Ala Gln Asp Ala Lys Ala Asp Ser Ala Tyr Val
20 25 30

Arg Asp Asn Tyr Glu Lys Ile Glu Gln Val Ile Pro Met Arg Asp Gly
35 40 45

Thr Lys Leu Phe Thr Ala Ile Tyr Gln Pro Lys Asp Lys Thr Lys Gln
50 55 60

Tyr Pro Val Leu Leu Asn Arg Thr Pro Tyr Thr Val Ala Pro Tyr Gly
65 70 75 80

Val Asn Glu Tyr Lys Lys Ser Leu Gly Asn Phe Pro Thr Glu Met Arg
85 90 95

Glu Gly Phe Ile Phe Val Tyr Gln Asp Val Arg Gly Lys Trp Met Ser
100 105 110

Glu Gly Glu Phe Glu Asp Val Arg Pro Ile Asn Pro Ser Lys Ser Lys

115

120

125

Lys Ala Ile Asp Glu Ser Thr Asp Thr Phe Asp Thr Leu Glu Trp Leu
 130 135 140

Ala Lys Asn Leu Lys Asn Tyr Thr Lys Lys Ala Gly Ile Tyr Gly Ile
 145 150 155 160

Ser Tyr Pro Gly Phe Tyr Ser Thr Met Ser Leu Val Asn Ser His Pro
 165 170 175

Thr Leu Lys Ala Val Ser Pro Gln Ala Pro Val Thr Asn Trp Phe Leu
 180 185 190

Gly Asp Asp Phe His His Asn Gly Val Leu Phe Leu Asn Asp Ser Phe
 195 200 205

Ser Phe Met Thr Phe Phe Gly Val Lys Arg Pro Gln Pro Ile Thr Pro
 210 215 220

Asp Lys Gly Pro Lys Arg Phe Glu Tyr Pro Ile Lys Asp Asn Tyr Arg
 225 230 235 240

Phe Tyr Ala Ser Gly Ser Val Lys Glu Leu Lys Asp Lys Tyr Leu Gln
 245 250 255

Asp Asn Ile Lys Phe Tyr Asn Asp Leu Phe Ala His Pro Asp Tyr Asp
 260 265 270

Gln Phe Trp Gln Asp Arg Asn Val Leu Pro His Leu Thr Asn Val Gln
 275 280 285

Pro Ala Val Met Thr Val Gly Gly Phe Phe Asp Ala Glu Asp Val Tyr
 290 295 300

Gly Ala Phe Glu Thr Tyr Lys Ala Ile Glu Lys Gln Asn Pro Lys Ala
 305 310 315 320

Thr Asn Ile Met Val Ala Gly Pro Trp Phe His Gly Gly Trp Val Arg

325

330

335

Ser Asn Gly Ser Thr Phe Gly Asp Met Gln Phe Ala Ser Asn Thr Ser
 340 345 350

Glu His Tyr Gln Gln Glu Ile Glu Leu Pro Phe Phe Asn Tyr Tyr Leu
 355 360 365

Lys Asp Lys Gly Asn Phe Lys Pro Thr Glu Ala Thr Ile Phe Ile Thr
 370 375 380

Gly Ser Asn Glu Trp Lys Gln Phe Asp Ala Trp Pro Pro Lys Asn Val
 385 390 395 400

Thr Thr Gln Lys Ile Tyr Leu Gln Gln Asn Gly Lys Ile Ala Phe Asn
 405 410 415

Lys Thr Asn Thr Thr Thr Thr Phe Asp Glu Tyr Val Ala Asp Pro Asn
 420 425 430

Ser Pro Val Pro Tyr Ser Gly Gly Val Leu Glu Thr Arg Ser Arg Glu
 435 440 445

Tyr Met Val Asp Asp Gln Arg Phe Ala Ser Thr Arg Pro Asp Val Met
 450 455 460

Val Tyr Gln Ser Asp Ile Leu Thr Glu Asp Ile Thr Leu Ala Gly Pro
 465 470 475 480

Val Ile Asn His Leu Val Val Ser Thr Thr Gly Thr Asp Ala Asp Tyr
 485 490 495

Val Val Lys Leu Ile Asp Val Tyr Pro Glu Asn Thr Pro Lys Phe Asn
 500 505 510

Asn Lys Leu Met Ala Gly Tyr Gln Asn Leu Ile Arg Ala Glu Ile Met
 515 520 525

Arg Gly Lys Tyr Arg Asn Ser Phe Ser Asn Pro Glu Ala Met Val Pro

530

535

540

Asn Lys Glu Thr Asn Val Thr Tyr Thr Met Pro Asp Val Gly His Thr
 545 550 555 560

Phe Lys Lys Gly His Arg Ile Met Ile Gln Val Gln Asn Ser Trp Phe
 565 570 575

Pro Leu Ala Asp Arg Asn Pro Gln Gln Phe Met Asn Val Tyr Glu Ala
 580 585 590

Thr Ser Lys Asp Tyr Leu Lys Gln Thr Gln Arg Ile Tyr His Thr Ser
 595 600 605

Tyr Ile Glu Ile Pro Val Leu Lys
 610 615

<210> 7
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 7
 gtatcacgag gccctagctg tgggtgtcatg gtcggtgatc

40

<210> 8
 <211> 40
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 8
 ttcgggggatt ccatatgata cccttttttac gtgaacttgc

40

<210> 9
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 9
 gggaattcca tatgaaaaaa ttaacattaa aagtaact 38

<210> 10
 <211> 36
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 10
 gggggctgca gtacttgtac ggtttcgccc gataaa 36

<210> 11
 <211> 1935
 <212> DNA
 <213> Sphingobacterium sp.

<220>
 <221> CDS
 <222> (61)..(1917)
 <223>

<400> 11
 gaaaccaagt gtaaaattat aatttacacc aaagaatgta ctgaacaaat aattatctga 60

atg aaa aat aca att tcg tgc cta act tta gcg ctt tta agc gca agc 108
 Met Lys Asn Thr Ile Ser Cys Leu Thr Leu Ala Leu Leu Ser Ala Ser
 1 5 10 15

cag tta cat gct caa aca gct gcc gac tcg gct tat gtt aga gat cat 156
 Gln Leu His Ala Gln Thr Ala Ala Asp Ser Ala Tyr Val Arg Asp His
 20 25 30

tat gaa aag acc gaa gta gca att ccc atg cga gat ggg aaa aaa tta 204
 Tyr Glu Lys Thr Glu Val Ala Ile Pro Met Arg Asp Gly Lys Lys Leu
 35 40 45

ttt act gcg atc tac agt cca aaa gac aaa tcc aag aaa tat cca gtt 252
 Phe Thr Ala Ile Tyr Ser Pro Lys Asp Lys Ser Lys Lys Tyr Pro Val
 50 55 60

ttg ctc aat aga acg ccc tac acg gtt tca cct tat ggg cag aac gaa 300
 Leu Leu Asn Arg Thr Pro Tyr Thr Val Ser Pro Tyr Gly Gln Asn Glu
 65 70 75 80

tat	aaa	aaa	agc	ttg	gga	aac	ttt	ccc	caa	atg	atg	cgt	gaa	ggc	tat	348
Tyr	Lys	Lys	Ser	Leu	Gly	Asn	Phe	Pro	Gln	Met	Met	Arg	Glu	Gly	Tyr	
			85					90						95		
att	ttc	gtt	tac	cag	gat	gtc	cgt	ggc	aag	tgg	atg	agc	gaa	ggg	gat	396
Ile	Phe	Val	Tyr	Gln	Asp	Val	Arg	Gly	Lys	Trp	Met	Ser	Glu	Gly	Asp	
			100					105					110			
ttt	gaa	gat	ata	cgt	ccg	acc	acg	tac	agc	aaa	gat	aaa	aaa	gca	atc	444
Phe	Glu	Asp	Ile	Arg	Pro	Thr	Thr	Tyr	Ser	Lys	Asp	Lys	Lys	Ala	Ile	
		115					120					125				
gat	gaa	agt	acg	gat	acc	tat	gat	gcg	ctt	gaa	tgg	tta	cag	aaa	aat	492
Asp	Glu	Ser	Thr	Asp	Thr	Tyr	Asp	Ala	Leu	Glu	Trp	Leu	Gln	Lys	Asn	
	130					135					140					
ctc	aaa	aac	tat	aat	ggc	aaa	gcc	ggg	ctc	tat	ggg	att	tcc	tat	cca	540
Leu	Lys	Asn	Tyr	Asn	Gly	Lys	Ala	Gly	Leu	Tyr	Gly	Ile	Ser	Tyr	Pro	
145					150				155						160	
ggc	ttc	tat	tct	acc	gtc	gga	ttg	gtc	aaa	aca	cac	ccg	agc	ttg	aag	588
Gly	Phe	Tyr	Ser	Thr	Val	Gly	Leu	Val	Lys	Thr	His	Pro	Ser	Leu	Lys	
				165				170						175		
gca	gtc	tcc	cca	cag	gct	ccc	gta	aca	gac	tgg	tat	atc	ggc	gac	gac	636
Ala	Val	Ser	Pro	Gln	Ala	Pro	Val	Thr	Asp	Trp	Tyr	Ile	Gly	Asp	Asp	
			180					185					190			
ttc	cac	cat	aat	ggc	gta	ttg	ttt	ctt	cag	gat	gca	ttt	aca	ttc	atg	684
Phe	His	His	Asn	Gly	Val	Leu	Phe	Leu	Gln	Asp	Ala	Phe	Thr	Phe	Met	
		195					200					205				
tca	acc	ttt	ggg	gtc	cct	cgt	cca	aaa	ccc	att	aca	ccg	gat	caa	ttt	732
Ser	Thr	Phe	Gly	Val	Pro	Arg	Pro	Lys	Pro	Ile	Thr	Pro	Asp	Gln	Phe	
	210					215					220					
aag	ggc	aaa	att	cag	atc	aaa	gaa	gcc	gat	aaa	tat	aac	ttt	ttt	gca	780
Lys	Gly	Lys	Ile	Gln	Ile	Lys	Glu	Ala	Asp	Lys	Tyr	Asn	Phe	Phe	Ala	
225					230				235						240	
gaa	gca	gga	aca	gcg	cgg	gaa	ctc	aaa	gaa	aag	tat	ttt	ggg	gac	tcc	828
Glu	Ala	Gly	Thr	Ala	Arg	Glu	Leu	Lys	Glu	Lys	Tyr	Phe	Gly	Asp	Ser	
				245					250					255		
gta	caa	ttt	tgg	aat	gac	ctg	ttt	aag	cat	ccc	gac	tat	gat	gat	ttt	876
Val	Gln	Phe	Trp	Asn	Asp	Leu	Phe	Lys	His	Pro	Asp	Tyr	Asp	Asp	Phe	
			260					265					270			
tgg	aaa	tcg	cgt	gtg	atc	acg	aat	tct	tta	cag	gag	gta	aaa	cca	gct	924
Trp	Lys	Ser	Arg	Val	Ile	Thr	Asn	Ser	Leu	Gln	Glu	Val	Lys	Pro	Ala	
		275					280					285				

gtg	atg	gtg	gtt	ggg	ggg	ttc	ttt	gac	gcg	gaa	gat	gct	tat	gga	aca	972
Val	Met	Val	Val	Gly	Gly	Phe	Phe	Asp	Ala	Glu	Asp	Ala	Tyr	Gly	Thr	
290						295					300					
ttt	aag	acc	tac	caa	tcg	att	gag	gat	aaa	agc	aaa	aaa	aac	aac	tcg	1020
Phe	Lys	Thr	Tyr	Gln	Ser	Ile	Glu	Asp	Lys	Ser	Lys	Lys	Asn	Asn	Ser	
305					310					315					320	
att	tta	gtc	gcg	gga	cct	tgg	tat	cat	ggc	ggg	tgg	gtt	cgt	gca	gaa	1068
Ile	Leu	Val	Ala	Gly	Pro	Trp	Tyr	His	Gly	Gly	Trp	Val	Arg	Ala	Glu	
				325					330					335		
gga	aac	tat	tta	ggg	gat	atc	caa	ttt	gag	aaa	aaa	acc	agt	att	act	1116
Gly	Asn	Tyr	Leu	Gly	Asp	Ile	Gln	Phe	Glu	Lys	Lys	Thr	Ser	Ile	Thr	
			340					345					350			
tat	cag	gaa	caa	ttt	gaa	caa	cca	ttt	ttc	aaa	tat	tac	cta	aaa	gat	1164
Tyr	Gln	Glu	Gln	Phe	Glu	Gln	Pro	Phe	Phe	Lys	Tyr	Tyr	Leu	Lys	Asp	
		355					360					365				
gaa	gga	aac	ttc	gcc	cct	tcc	gaa	gct	aac	att	ttt	gtt	tca	ggc	agc	1212
Glu	Gly	Asn	Phe	Ala	Pro	Ser	Glu	Ala	Asn	Ile	Phe	Val	Ser	Gly	Ser	
	370					375					380					
aac	gaa	tgg	aaa	cat	ttc	gaa	cag	tgg	cca	cca	aaa	aat	gta	gag	aca	1260
Asn	Glu	Trp	Lys	His	Phe	Glu	Gln	Trp	Pro	Pro	Lys	Asn	Val	Glu	Thr	
385					390					395					400	
aaa	aaa	cta	tac	ttc	caa	cct	cag	ggg	aaa	ctt	gga	ttt	gac	aaa	gtt	1308
Lys	Lys	Leu	Tyr	Phe	Gln	Pro	Gln	Gly	Lys	Leu	Gly	Phe	Asp	Lys	Val	
				405					410					415		
caa	cgt	aca	gat	tcc	tgg	gat	gaa	tat	gta	aca	gac	cct	aat	aaa	cct	1356
Gln	Arg	Thr	Asp	Ser	Trp	Asp	Glu	Tyr	Val	Thr	Asp	Pro	Asn	Lys	Pro	
			420					425					430			
gtt	ccg	cat	caa	ggg	ggg	gta	att	caa	aac	cga	aca	cgg	gag	tat	atg	1404
Val	Pro	His	Gln	Gly	Gly	Val	Ile	Gln	Asn	Arg	Thr	Arg	Glu	Tyr	Met	
		435					440					445				
gta	gat	gat	caa	cgt	ttc	gcg	gct	agt	cgc	cct	gat	gtc	atg	gtt	tat	1452
Val	Asp	Asp	Gln	Arg	Phe	Ala	Ala	Ser	Arg	Pro	Asp	Val	Met	Val	Tyr	
	450					455					460					
caa	acg	gaa	ccg	ttg	acg	gag	gac	ctg	acg	ata	gta	ggc	cca	atc	aaa	1500
Gln	Thr	Glu	Pro	Leu	Thr	Glu	Asp	Leu	Thr	Ile	Val	Gly	Pro	Ile	Lys	
465					470					475					480	
aac	ttt	ctc	aaa	gtt	tct	tca	aca	gga	aca	gac	gcg	gac	tat	gtt	gtc	1548
Asn	Phe	Leu	Lys	Val	Ser	Ser	Thr	Gly	Thr	Asp	Ala	Asp	Tyr	Val	Val	
				485					490					495		

aaa ctg att gac gtt tat ccg aat gat gca gca agt tat caa gga aaa	1596
Lys Leu Ile Asp Val Tyr Pro Asn Asp Ala Ala Ser Tyr Gln Gly Lys	
500 505 510	
aca atg gct gga tat caa atg atg gta cgt ggt gag atc atg gcg ggg	1644
Thr Met Ala Gly Tyr Gln Met Met Val Arg Gly Glu Ile Met Ala Gly	
515 520 525	
aaa tac cga aat ggt ttc gat aaa gcg cag gcc ttg act cca ggt atg	1692
Lys Tyr Arg Asn Gly Phe Asp Lys Ala Gln Ala Leu Thr Pro Gly Met	
530 535 540	
gtc gaa aag gtg aat ttt gaa atg cca gac gtt gcg cat acc ttc aaa	1740
Val Glu Lys Val Asn Phe Glu Met Pro Asp Val Ala His Thr Phe Lys	
545 550 555 560	
aaa gga cat cgc att atg gtt cag gta caa aac tca tgg ttt ccg ctg	1788
Lys Gly His Arg Ile Met Val Gln Val Gln Asn Ser Trp Phe Pro Leu	
565 570 575	
gca gaa cga aat cca cag gtg ttt tta gca cct tat aca gct acc aaa	1836
Ala Glu Arg Asn Pro Gln Val Phe Leu Ala Pro Tyr Thr Ala Thr Lys	
580 585 590	
gct gat ttc cgc aaa gct acc caa cgt att ttt cac gat gtg aac aat	1884
Ala Asp Phe Arg Lys Ala Thr Gln Arg Ile Phe His Asp Val Asn Asn	
595 600 605	
gcc aca tac atc gaa ttt tct gtc ctc aaa gat tagcaggtaa attcgaaa	1935
Ala Thr Tyr Ile Glu Phe Ser Val Leu Lys Asp	
610 615	

<210> 12
 <211> 619
 <212> PRT
 <213> Sphingobacterium sp.

<400> 12

Met Lys Asn Thr Ile Ser Cys Leu Thr Leu Ala Leu Leu Ser Ala Ser	
1 5 10 15	
Gln Leu His Ala Gln Thr Ala Ala Asp Ser Ala Tyr Val Arg Asp His	
20 25 30	
Tyr Glu Lys Thr Glu Val Ala Ile Pro Met Arg Asp Gly Lys Lys Leu	
35 40 45	

Phe	Thr	Ala	Ile	Tyr	Ser	Pro	Lys	Asp	Lys	Ser	Lys	Lys	Tyr	Pro	Val	50	55	60	
Leu	Leu	Asn	Arg	Thr	Pro	Tyr	Thr	Val	Ser	Pro	Tyr	Gly	Gln	Asn	Glu	65	70	75	80
Tyr	Lys	Lys	Ser	Leu	Gly	Asn	Phe	Pro	Gln	Met	Met	Arg	Glu	Gly	Tyr	85	90	95	
Ile	Phe	Val	Tyr	Gln	Asp	Val	Arg	Gly	Lys	Trp	Met	Ser	Glu	Gly	Asp	100	105	110	
Phe	Glu	Asp	Ile	Arg	Pro	Thr	Thr	Tyr	Ser	Lys	Asp	Lys	Lys	Ala	Ile	115	120	125	
Asp	Glu	Ser	Thr	Asp	Thr	Tyr	Asp	Ala	Leu	Glu	Trp	Leu	Gln	Lys	Asn	130	135	140	
Leu	Lys	Asn	Tyr	Asn	Gly	Lys	Ala	Gly	Leu	Tyr	Gly	Ile	Ser	Tyr	Pro	145	150	155	160
Gly	Phe	Tyr	Ser	Thr	Val	Gly	Leu	Val	Lys	Thr	His	Pro	Ser	Leu	Lys	165	170	175	
Ala	Val	Ser	Pro	Gln	Ala	Pro	Val	Thr	Asp	Trp	Tyr	Ile	Gly	Asp	Asp	180	185	190	
Phe	His	His	Asn	Gly	Val	Leu	Phe	Leu	Gln	Asp	Ala	Phe	Thr	Phe	Met	195	200	205	
Ser	Thr	Phe	Gly	Val	Pro	Arg	Pro	Lys	Pro	Ile	Thr	Pro	Asp	Gln	Phe	210	215	220	
Lys	Gly	Lys	Ile	Gln	Ile	Lys	Glu	Ala	Asp	Lys	Tyr	Asn	Phe	Phe	Ala	225	230	235	240
Glu	Ala	Gly	Thr	Ala	Arg	Glu	Leu	Lys	Glu	Lys	Tyr	Phe	Gly	Asp	Ser	245	250	255	

Val Gln Phe Trp Asn Asp Leu Phe Lys His Pro Asp Tyr Asp Asp Phe
 260 265 270

Trp Lys Ser Arg Val Ile Thr Asn Ser Leu Gln Glu Val Lys Pro Ala
 275 280 285

Val Met Val Val Gly Gly Phe Phe Asp Ala Glu Asp Ala Tyr Gly Thr
 290 295 300

Phe Lys Thr Tyr Gln Ser Ile Glu Asp Lys Ser Lys Lys Asn Asn Ser
 305 310 315 320

Ile Leu Val Ala Gly Pro Trp Tyr His Gly Gly Trp Val Arg Ala Glu
 325 330 335

Gly Asn Tyr Leu Gly Asp Ile Gln Phe Glu Lys Lys Thr Ser Ile Thr
 340 345 350

Tyr Gln Glu Gln Phe Glu Gln Pro Phe Phe Lys Tyr Tyr Leu Lys Asp
 355 360 365

Glu Gly Asn Phe Ala Pro Ser Glu Ala Asn Ile Phe Val Ser Gly Ser
 370 375 380

Asn Glu Trp Lys His Phe Glu Gln Trp Pro Pro Lys Asn Val Glu Thr
 385 390 395 400

Lys Lys Leu Tyr Phe Gln Pro Gln Gly Lys Leu Gly Phe Asp Lys Val
 405 410 415

Gln Arg Thr Asp Ser Trp Asp Glu Tyr Val Thr Asp Pro Asn Lys Pro
 420 425 430

Val Pro His Gln Gly Gly Val Ile Gln Asn Arg Thr Arg Glu Tyr Met
 435 440 445

Val Asp Asp Gln Arg Phe Ala Ala Ser Arg Pro Asp Val Met Val Tyr
 450 455 460

Gln Thr Glu Pro Leu Thr Glu Asp Leu Thr Ile Val Gly Pro Ile Lys
 465 470 475 480

Asn Phe Leu Lys Val Ser Ser Thr Gly Thr Asp Ala Asp Tyr Val Val
 485 490 495

Lys Leu Ile Asp Val Tyr Pro Asn Asp Ala Ala Ser Tyr Gln Gly Lys
 500 505 510

Thr Met Ala Gly Tyr Gln Met Met Val Arg Gly Glu Ile Met Ala Gly
 515 520 525

Lys Tyr Arg Asn Gly Phe Asp Lys Ala Gln Ala Leu Thr Pro Gly Met
 530 535 540

Val Glu Lys Val Asn Phe Glu Met Pro Asp Val Ala His Thr Phe Lys
 545 550 555 560

Lys Gly His Arg Ile Met Val Gln Val Gln Asn Ser Trp Phe Pro Leu
 565 570 575

Ala Glu Arg Asn Pro Gln Val Phe Leu Ala Pro Tyr Thr Ala Thr Lys
 580 585 590

Ala Asp Phe Arg Lys Ala Thr Gln Arg Ile Phe His Asp Val Asn Asn
 595 600 605

Ala Thr Tyr Ile Glu Phe Ser Val Leu Lys Asp
 610 615

<210> 13
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 13
 gggaattcca tatgaaaaat acaatttcgt

<210> 14
 <211> 29
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic DNA

 <400> 14
 gctctagact aatctttgag gacagaaaa 29

 <210> 15
 <211> 17
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic DNA

 <400> 15
 gaygayttyc aycayaa 17

 <210> 16
 <211> 20
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Synthetic DNA

 <220>
 <221> misc_feature
 <222> (9)..(9)
 <223> n = a, c, g, or t

 <400> 16
 tgrtcrtcna ccatrtaytc 20

 <210> 17
 <211> 1974
 <212> DNA
 <213> Pedobacter heparinus

 <220>
 <221> CDS
 <222> (61)..(1935)
 <223>

<400> 17

aaacctatcc	cgtattcagc	aatcaattcc	atatatttat	ccttaaaaaa	accttcctct	60
atg act cct ttc aaa tcg ttc tcc ttc att ttt ctc ttt att ttt acc	108					
Met Thr Pro Phe Lys Ser Phe Ser Phe Ile Phe Leu Phe Ile Phe Thr						
1 5 10 15						
agt ctt tct gct tct gca caa cag tcc gac tct gct tat ata cgt cag	156					
Ser Leu Ser Ala Ser Ala Gln Gln Ser Asp Ser Ala Tyr Ile Arg Gln						
20 25 30						
aac tat acc aaa ata gaa agg ctg atc cct atg cgg gat ggc att aag	204					
Asn Tyr Thr Lys Ile Glu Arg Leu Ile Pro Met Arg Asp Gly Ile Lys						
35 40 45						
cta ttt aca gcc att tac atc ccc aaa gac aaa agc aag aag tat cct	252					
Leu Phe Thr Ala Ile Tyr Ile Pro Lys Asp Lys Ser Lys Lys Tyr Pro						
50 55 60						
ttt atg ctc aac cgt act cct tat acc gtt tcg cct tat ggc gaa aac	300					
Phe Met Leu Asn Arg Thr Pro Tyr Thr Val Ser Pro Tyr Gly Glu Asn						
65 70 75 80						
aat tat aaa aca agc ctt ggc ccc tct ccg ctc ttt ata aaa gaa ggc	348					
Asn Tyr Lys Thr Ser Leu Gly Pro Ser Pro Leu Phe Ile Lys Glu Gly						
85 90 95						
ttt atc ttt gtt tat cag gat gta agg ggc aaa tgg atg agt gag gga	396					
Phe Ile Phe Val Tyr Gln Asp Val Arg Gly Lys Trp Met Ser Glu Gly						
100 105 110						
aaa ttt gaa gac gta agg ccg caa ata gcc agc aag aaa cgc aaa acg	444					
Lys Phe Glu Asp Val Arg Pro Gln Ile Ala Ser Lys Lys Arg Lys Thr						
115 120 125						
gat att gat gaa agc tcc gat act tat gat acg atc gac tgg ctg atc	492					
Asp Ile Asp Glu Ser Ser Asp Thr Tyr Asp Thr Ile Asp Trp Leu Ile						
130 135 140						
agg aac att cct gga aac aac cgt aaa acc ggt att tac ggt atc tca	540					
Arg Asn Ile Pro Gly Asn Asn Arg Lys Thr Gly Ile Tyr Gly Ile Ser						
145 150 155 160						
tac cca ggc ttt tat gct act gct gcc cta cca gat gcg cat cca tct	588					
Tyr Pro Gly Phe Tyr Ala Thr Ala Ala Leu Pro Asp Ala His Pro Ser						
165 170 175						
tta aag gca gta tcg ccc cag gct ccg gtt acc gac tgg ttt ata ggc	636					
Leu Lys Ala Val Ser Pro Gln Ala Pro Val Thr Asp Trp Phe Ile Gly						
180 185 190						
gat gat ttt cat cac aat ggc acc ttg ttc ctt gca gat atc ttt agc	684					

Asp	Asp	Phe	His	His	Asn	Gly	Thr	Leu	Phe	Leu	Ala	Asp	Ile	Phe	Ser	
		195					200					205				
ttc	tat	tat	acc	ttc	ggg	gta	ccg	cga	cct	caa	cca	att	acg	ccc	gac	732
Phe	Tyr	Tyr	Thr	Phe	Gly	Val	Pro	Arg	Pro	Gln	Pro	Ile	Thr	Pro	Asp	
	210					215					220					
aaa	cgt	cca	aaa	ccc	ttt	gat	ttc	ccg	gtt	aaa	gac	aac	tac	cgt	ttt	780
Lys	Arg	Pro	Lys	Pro	Phe	Asp	Phe	Pro	Val	Lys	Asp	Asn	Tyr	Arg	Phe	
225					230					235					240	
ttt	ctt	gaa	ctg	ggc	ccc	tta	aaa	aac	atc	acc	aaa	aaa	tat	tat	ggc	828
Phe	Leu	Glu	Leu	Gly	Pro	Leu	Lys	Asn	Ile	Thr	Lys	Lys	Tyr	Tyr	Gly	
				245					250					255		
gat	acc	ata	cga	ttc	tgg	aat	gat	atc	aat	gcg	cat	acc	aat	tat	gat	876
Asp	Thr	Ile	Arg	Phe	Trp	Asn	Asp	Ile	Asn	Ala	His	Thr	Asn	Tyr	Asp	
			260					265					270			
gcc	ttc	tgg	aaa	gcc	cgt	aac	att	acg	ccg	cat	tta	att	ggg	gta	aaa	924
Ala	Phe	Trp	Lys	Ala	Arg	Asn	Ile	Thr	Pro	His	Leu	Ile	Gly	Val	Lys	
		275					280					285				
cct	gca	gtt	ttg	gta	gtt	ggc	ggc	ttc	ttt	gat	gca	gaa	gac	ctt	tac	972
Pro	Ala	Val	Leu	Val	Val	Gly	Gly	Phe	Phe	Asp	Ala	Glu	Asp	Leu	Tyr	
	290					295					300					
ggg	acg	ctt	aaa	acc	tat	cag	gcc	atc	gaa	aaa	caa	aat	cca	tcc	tca	1020
Gly	Thr	Leu	Lys	Thr	Tyr	Gln	Ala	Ile	Glu	Lys	Gln	Asn	Pro	Ser	Ser	
305					310					315					320	
aaa	aac	aac	ctc	gtt	atg	ggc	ccc	tgg	tac	cat	ggg	ggc	tgg	gca	aga	1068
Lys	Asn	Asn	Leu	Val	Met	Gly	Pro	Trp	Tyr	His	Gly	Gly	Trp	Ala	Arg	
				325					330					335		
agt	acg	gga	agc	agt	ttc	ggg	gat	att	aat	ttc	gga	cag	cca	acc	agt	1116
Ser	Thr	Gly	Ser	Ser	Phe	Gly	Asp	Ile	Asn	Phe	Gly	Gln	Pro	Thr	Ser	
			340					345					350			
act	tca	tac	cag	caa	aat	gtt	gag	ttc	cct	ttc	ttt	atg	caa	tac	ctc	1164
Thr	Ser	Tyr	Gln	Gln	Asn	Val	Glu	Phe	Pro	Phe	Phe	Met	Gln	Tyr	Leu	
		355					360					365				
aaa	gag	gca	ccg	gat	gca	aaa	att	gca	gag	gca	acc	att	ttt	atc	act	1212
Lys	Glu	Ala	Pro	Asp	Ala	Lys	Ile	Ala	Glu	Ala	Thr	Ile	Phe	Ile	Thr	
	370					375					380					
ggc	agc	aat	gaa	tgg	aag	aaa	ttt	agc	tcc	tgg	cca	cct	cag	gat	aca	1260
Gly	Ser	Asn	Glu	Trp	Lys	Lys	Phe	Ser	Ser	Trp	Pro	Pro	Gln	Asp	Thr	
385					390					395					400	
gaa	gaa	aga	aca	tta	tac	ctg	cag	ccc	aat	ggc	aaa	ctg	agc	ttt	gag	1308

Glu	Glu	Arg	Thr	Leu	Tyr	Leu	Gln	Pro	Asn	Gly	Lys	Leu	Ser	Phe	Glu	
				405					410					415		
aag	gta	cag	cgg	acc	gac	agc	tgg	gat	gaa	tat	gta	agt	gat	ccc	aat	1356
Lys	Val	Gln	Arg	Thr	Asp	Ser	Trp	Asp	Glu	Tyr	Val	Ser	Asp	Pro	Asn	
			420					425					430			
tca	cct	gtc	cct	tat	cag	gat	ggc	ata	caa	acc	agc	aga	acc	cgg	gaa	1404
Ser	Pro	Val	Pro	Tyr	Gln	Asp	Gly	Ile	Gln	Thr	Ser	Arg	Thr	Arg	Glu	
			435				440					445				
tat	atg	atc	gat	gac	cag	cgt	ttt	gcc	tcg	cgc	aga	ccg	gat	gta	agg	1452
Tyr	Met	Ile	Asp	Asp	Gln	Arg	Phe	Ala	Ser	Arg	Arg	Pro	Asp	Val	Arg	
	450					455					460					
gta	ttc	caa	aca	gag	ccc	ctc	agt	tcc	gac	ctt	aca	ctt	acc	ggc	ccg	1500
Val	Phe	Gln	Thr	Glu	Pro	Leu	Ser	Ser	Asp	Leu	Thr	Leu	Thr	Gly	Pro	
465				470						475				480		
gta	ttg	gcc	aaa	ctg	gtg	gta	tca	acc	aca	ggc	acg	gat	gca	gat	tat	1548
Val	Leu	Ala	Lys	Leu	Val	Val	Ser	Thr	Thr	Gly	Thr	Asp	Ala	Asp	Tyr	
				485					490				495			
gtg	gta	aaa	ctg	ata	gat	gta	tat	ccg	gaa	gat	aca	cca	aat	cct	gta	1596
Val	Val	Lys	Leu	Ile	Asp	Val	Tyr	Pro	Glu	Asp	Thr	Pro	Asn	Pro	Val	
			500					505					510			
cct	aac	cct	aaa	aac	ctg	atc	atg	ggc	ggc	tac	cag	atg	ctg	gta	cgc	1644
Pro	Asn	Pro	Lys	Asn	Leu	Ile	Met	Gly	Gly	Tyr	Gln	Met	Leu	Val	Arg	
			515				520					525				
ggc	gag	atc	atg	cgt	gga	aaa	tac	cgt	aac	agc	ttt	gaa	aaa	ccc	gag	1692
Gly	Glu	Ile	Met	Arg	Gly	Lys	Tyr	Arg	Asn	Ser	Phe	Glu	Lys	Pro	Glu	
	530					535					540					
cct	ttt	gtt	cct	gga	aca	att	aca	aaa	gta	aac	tat	gcc	ctt	ccg	gat	1740
Pro	Phe	Val	Pro	Gly	Thr	Ile	Thr	Lys	Val	Asn	Tyr	Ala	Leu	Pro	Asp	
545				550						555				560		
gta	gcc	cat	acc	ttt	aaa	aaa	ggc	cac	cgc	atc	atg	atc	cag	gtc	cag	1788
Val	Ala	His	Thr	Phe	Lys	Lys	Gly	His	Arg	Ile	Met	Ile	Gln	Val	Gln	
				565					570				575			
aat	tca	tgg	ttt	ccc	ctg	gcc	gac	cgg	aat	cca	cag	cag	ttt	atg	gac	1836
Asn	Ser	Trp	Phe	Pro	Leu	Ala	Asp	Arg	Asn	Pro	Gln	Gln	Phe	Met	Asp	
			580					585					590			
att	tac	cag	gcc	gaa	cct	ggc	gat	ttc	aga	aaa	gct	acg	cat	agg	atc	1884
Ile	Tyr	Gln	Ala	Glu	Pro	Gly	Asp	Phe	Arg	Lys	Ala	Thr	His	Arg	Ile	
			595				600					605				
ttc	cac	gat	gta	cac	aat	gca	tct	gca	att	acg	gta	aac	gta	ctg	aaa	1932

Phe His Asp Val His Asn Ala Ser Ala Ile Thr Val Asn Val Leu Lys
610 615 620

cct taaaacggat gaaaccagta tattgtgccca tccttactt

1974

Pro
625

<210> 18
<211> 625
<212> PRT
<213> Pedobacter heparinus

<400> 18

Met Thr Pro Phe Lys Ser Phe Ser Phe Ile Phe Leu Phe Ile Phe Thr
1 5 10 15

Ser Leu Ser Ala Ser Ala Gln Gln Ser Asp Ser Ala Tyr Ile Arg Gln
20 25 30

Asn Tyr Thr Lys Ile Glu Arg Leu Ile Pro Met Arg Asp Gly Ile Lys
35 40 45

Leu Phe Thr Ala Ile Tyr Ile Pro Lys Asp Lys Ser Lys Lys Tyr Pro
50 55 60

Phe Met Leu Asn Arg Thr Pro Tyr Thr Val Ser Pro Tyr Gly Glu Asn
65 70 75 80

Asn Tyr Lys Thr Ser Leu Gly Pro Ser Pro Leu Phe Ile Lys Glu Gly
85 90 95

Phe Ile Phe Val Tyr Gln Asp Val Arg Gly Lys Trp Met Ser Glu Gly
100 105 110

Lys Phe Glu Asp Val Arg Pro Gln Ile Ala Ser Lys Lys Arg Lys Thr
115 120 125

Asp Ile Asp Glu Ser Ser Asp Thr Tyr Asp Thr Ile Asp Trp Leu Ile
130 135 140

Arg Asn Ile Pro Gly Asn Asn Arg Lys Thr Gly Ile Tyr Gly Ile Ser

145		150		155		160									
Tyr	Pro	Gly	Phe	Tyr	Ala	Thr	Ala	Ala	Leu	Pro	Asp	Ala	His	Pro	Ser
				165					170					175	
Leu	Lys	Ala	Val	Ser	Pro	Gln	Ala	Pro	Val	Thr	Asp	Trp	Phe	Ile	Gly
			180					185					190		
Asp	Asp	Phe	His	His	Asn	Gly	Thr	Leu	Phe	Leu	Ala	Asp	Ile	Phe	Ser
		195					200					205			
Phe	Tyr	Tyr	Thr	Phe	Gly	Val	Pro	Arg	Pro	Gln	Pro	Ile	Thr	Pro	Asp
	210					215					220				
Lys	Arg	Pro	Lys	Pro	Phe	Asp	Phe	Pro	Val	Lys	Asp	Asn	Tyr	Arg	Phe
225					230					235					240
Phe	Leu	Glu	Leu	Gly	Pro	Leu	Lys	Asn	Ile	Thr	Lys	Lys	Tyr	Tyr	Gly
				245					250					255	
Asp	Thr	Ile	Arg	Phe	Trp	Asn	Asp	Ile	Asn	Ala	His	Thr	Asn	Tyr	Asp
			260					265					270		
Ala	Phe	Trp	Lys	Ala	Arg	Asn	Ile	Thr	Pro	His	Leu	Ile	Gly	Val	Lys
		275					280					285			
Pro	Ala	Val	Leu	Val	Val	Gly	Gly	Phe	Phe	Asp	Ala	Glu	Asp	Leu	Tyr
	290					295					300				
Gly	Thr	Leu	Lys	Thr	Tyr	Gln	Ala	Ile	Glu	Lys	Gln	Asn	Pro	Ser	Ser
305					310					315					320
Lys	Asn	Asn	Leu	Val	Met	Gly	Pro	Trp	Tyr	His	Gly	Gly	Trp	Ala	Arg
				325					330					335	
Ser	Thr	Gly	Ser	Ser	Phe	Gly	Asp	Ile	Asn	Phe	Gly	Gln	Pro	Thr	Ser
			340					345					350		
Thr	Ser	Tyr	Gln	Gln	Asn	Val	Glu	Phe	Pro	Phe	Phe	Met	Gln	Tyr	Leu

355

360

365

Lys Glu Ala Pro Asp Ala Lys Ile Ala Glu Ala Thr Ile Phe Ile Thr
 370 375 380

Gly Ser Asn Glu Trp Lys Lys Phe Ser Ser Trp Pro Pro Gln Asp Thr
 385 390 395 400

Glu Glu Arg Thr Leu Tyr Leu Gln Pro Asn Gly Lys Leu Ser Phe Glu
 405 410 415

Lys Val Gln Arg Thr Asp Ser Trp Asp Glu Tyr Val Ser Asp Pro Asn
 420 425 430

Ser Pro Val Pro Tyr Gln Asp Gly Ile Gln Thr Ser Arg Thr Arg Glu
 435 440 445

Tyr Met Ile Asp Asp Gln Arg Phe Ala Ser Arg Arg Pro Asp Val Arg
 450 455 460

Val Phe Gln Thr Glu Pro Leu Ser Ser Asp Leu Thr Leu Thr Gly Pro
 465 470 475 480

Val Leu Ala Lys Leu Val Val Ser Thr Thr Gly Thr Asp Ala Asp Tyr
 485 490 495

Val Val Lys Leu Ile Asp Val Tyr Pro Glu Asp Thr Pro Asn Pro Val
 500 505 510

Pro Asn Pro Lys Asn Leu Ile Met Gly Gly Tyr Gln Met Leu Val Arg
 515 520 525

Gly Glu Ile Met Arg Gly Lys Tyr Arg Asn Ser Phe Glu Lys Pro Glu
 530 535 540

Pro Phe Val Pro Gly Thr Ile Thr Lys Val Asn Tyr Ala Leu Pro Asp
 545 550 555 560

Val Ala His Thr Phe Lys Lys Gly His Arg Ile Met Ile Gln Val Gln

565

570

575

Asn Ser Trp Phe Pro Leu Ala Asp Arg Asn Pro Gln Gln Phe Met Asp
 580 585 590

Ile Tyr Gln Ala Glu Pro Gly Asp Phe Arg Lys Ala Thr His Arg Ile
 595 600 605

Phe His Asp Val His Asn Ala Ser Ala Ile Thr Val Asn Val Leu Lys
 610 615 620

Pro
 625

<210> 19
 <211> 38
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 19
 gggaattcca tatgactcct ttcaaatcgt tctccttc

38

<210> 20
 <211> 30
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<400> 20
 cccaagcttt taaggtttca gtacgtttac

30

<210> 21
 <211> 17
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Synthetic DNA

<220>

<221> misc_feature
 <222> (9)..(9)
 <223> n = a, c, g, or t

<400> 21
 athttygtnt aycarga

17

<210> 22
 <211> 2018
 <212> DNA
 <213> Taxeobacter gelupurpurascens

<220>
 <221> CDS
 <222> (61)..(1995)
 <223>

<400> 22
 ctgaatgtct gctgacgaat tggaactaca ttaggctcgt tcttcaccta cccttcact

60

atg ccc tac tct ttc ccg aaa gtt gcc gcc ctg agt ggc cta ctg gtg
 Met Pro Tyr Ser Phe Pro Lys Val Ala Ala Leu Ser Gly Leu Leu Val
 1 5 10 15

108

gcc ggt tta tcc ggt gcc cac gcc caa act cct gtt acc tat ccg ctg
 Ala Gly Leu Ser Gly Ala His Ala Gln Thr Pro Val Thr Tyr Pro Leu
 20 25 30

156

gct tct gag gct gaa aaa gcg cag ctg gcg gtg gta cta gcc gat acg
 Ala Ser Glu Ala Glu Lys Ala Gln Leu Ala Val Val Leu Ala Asp Thr
 35 40 45

204

gct tac atc aag gag cgc tat acc aaa aca gaa tat cag att ccg atg
 Ala Tyr Ile Lys Glu Arg Tyr Thr Lys Thr Glu Tyr Gln Ile Pro Met
 50 55 60

252

cgc gat ggg gtg aag ttg tac acc att gtg tac gcg ccc aac gat gcc
 Arg Asp Gly Val Lys Leu Tyr Thr Ile Val Tyr Ala Pro Asn Asp Ala
 65 70 75 80

300

aac aag gta aag tac cct att ctg ctc aac cgt acc cct tac gct att
 Asn Lys Val Lys Tyr Pro Ile Leu Leu Asn Arg Thr Pro Tyr Ala Ile
 85 90 95

348

ggc ccc tac ggc ccc ggc aaa tac aag ctc aac ctg ggc ccc agc agc
 Gly Pro Tyr Gly Pro Gly Lys Tyr Lys Leu Asn Leu Gly Pro Ser Ser
 100 105 110

396

acg atg atg cat gag gga tac atc ttc gcc tac cag gat gtg cgt ggg
 Thr Met Met His Glu Gly Tyr Ile Phe Ala Tyr Gln Asp Val Arg Gly

444

115					120					125						
cga	tat	atg	tcg	gaa	gga	gag	ttt	gtg	gat	gtg	cgc	ccc	gaa	aag	gac	492
Arg	Tyr	Met	Ser	Glu	Gly	Glu	Phe	Val	Asp	Val	Arg	Pro	Glu	Lys	Asp	
	130					135					140					
atg	cac	aaa	ggc	aag	aac	gac	atc	gat	gaa	ggc	acc	gac	acc	tac	gat	540
Met	His	Lys	Gly	Lys	Asn	Asp	Ile	Asp	Glu	Gly	Thr	Asp	Thr	Tyr	Asp	
145					150					155					160	
acc	att	gag	tgg	ctt	ctg	aag	cac	ggg	ccc	aag	aat	aac	ggc	cgc	gta	588
Thr	Ile	Glu	Trp	Leu	Leu	Lys	His	Gly	Pro	Lys	Asn	Asn	Gly	Arg	Val	
				165					170					175		
ggc	cag	tgg	ggc	atc	tcc	tac	ccc	ggc	tac	tat	acc	gct	act	ggc	cta	636
Gly	Gln	Trp	Gly	Ile	Ser	Tyr	Pro	Gly	Tyr	Tyr	Thr	Ala	Thr	Gly	Leu	
			180					185					190			
ctg	agc	cgc	cac	aag	gcc	cta	aag	gca	tcc	tca	ccg	cag	gcc	cct	att	684
Leu	Ser	Arg	His	Lys	Ala	Leu	Lys	Ala	Ser	Ser	Pro	Gln	Ala	Pro	Ile	
		195					200					205				
gcc	gac	tgg	ttc	tgg	gac	gat	ttt	cac	cac	aac	ggc	gcg	ttc	ttc	ctg	732
Ala	Asp	Trp	Phe	Trp	Asp	Asp	Phe	His	His	Asn	Gly	Ala	Phe	Phe	Leu	
	210					215					220					
ccg	cac	gct	ttc	aac	ttc	ctg	gcc	tcc	ttt	ggg	ctg	gcc	cgc	ccc	cag	780
Pro	His	Ala	Phe	Asn	Phe	Leu	Ala	Ser	Phe	Gly	Leu	Ala	Arg	Pro	Gln	
225					230					235					240	
ccc	acg	cct	acc	ggc	aac	ccc	ggc	ttc	aag	cac	ggc	acc	ccc	gat	ggc	828
Pro	Thr	Pro	Thr	Gly	Asn	Pro	Gly	Phe	Lys	His	Gly	Thr	Pro	Asp	Gly	
				245					250					255		
tac	gat	ttt	ttc	ctg	aag	atg	ggc	ccg	ctg	aaa	aac	gct	gat	gcc	aac	876
Tyr	Asp	Phe	Phe	Leu	Lys	Met	Gly	Pro	Leu	Lys	Asn	Ala	Asp	Ala	Asn	
			260					265					270			
tac	tac	aaa	ggc	aaa	gtg	gcc	ttc	tgg	aac	gaa	atg	gcc	agc	cac	ccc	924
Tyr	Tyr	Lys	Gly	Lys	Val	Ala	Phe	Trp	Asn	Glu	Met	Ala	Ser	His	Pro	
		275					280					285				
aac	tac	gac	gaa	ttc	tgg	cag	gcc	cgt	aac	cta	cgc	ccc	cac	ctc	aag	972
Asn	Tyr	Asp	Glu	Phe	Trp	Gln	Ala	Arg	Asn	Leu	Arg	Pro	His	Leu	Lys	
	290					295					300					
aac	ctc	aac	aaa	ggc	acc	gcg	gtg	ctc	acg	gtt	ggc	ggc	ttc	aat	gat	1020
Asn	Leu	Asn	Lys	Gly	Thr	Ala	Val	Leu	Thr	Val	Gly	Gly	Phe	Asn	Asp	
305					310					315					320	
gcc	gag	gac	ctg	ttt	ggc	gcc	ctg	aaa	acc	tac	gaa	agc	atc	gag	aag	1068
Ala	Glu	Asp	Leu	Phe	Gly	Ala	Leu	Lys	Thr	Tyr	Glu	Ser	Ile	Glu	Lys	

325										330					335					
caa	aac	ccc	ggc	atg	cgc	aac	ggc	ctc	gtg	atg	ggg	ccg	tgg	gta	cac	1116				
Gln	Asn	Pro	Gly	Met	Arg	Asn	Gly	Leu	Val	Met	Gly	Pro	Trp	Val	His					
			340					345					350							
ggc	ggc	tgg	gcc	cgc	ggc	act	ggc	gaa	atg	gta	ggc	aat	gtg	gcc	tac	1164				
Gly	Gly	Trp	Ala	Arg	Gly	Thr	Gly	Glu	Met	Val	Gly	Asn	Val	Ala	Tyr					
		355					360					365								
ggc	gag	tcg	ccg	tcg	ttg	tat	tac	cag	aag	cag	att	gaa	gcg	ccg	ttc	1212				
Gly	Glu	Ser	Pro	Ser	Leu	Tyr	Tyr	Gln	Lys	Gln	Ile	Glu	Ala	Pro	Phe					
	370					375					380									
ttc	aaa	tca	tat	ctg	aag	gat	ggc	aaa	cct	gcc	gct	acc	ccc	gag	gct	1260				
Phe	Lys	Ser	Tyr	Leu	Lys	Asp	Gly	Lys	Pro	Ala	Ala	Thr	Pro	Glu	Ala					
385					390				395						400					
acc	atc	ttt	gaa	agc	ggc	acc	aac	cgc	tgg	cgc	agc	ttc	gaa	acc	tgg	1308				
Thr	Ile	Phe	Glu	Ser	Gly	Thr	Asn	Arg	Trp	Arg	Ser	Phe	Glu	Thr	Trp					
				405					410					415						
ccg	ccc	aaa	gaa	gcc	aaa	gag	cgc	act	ttg	tac	ttt	cag	tcg	gcc	ggg	1356				
Pro	Pro	Lys	Glu	Ala	Lys	Glu	Arg	Thr	Leu	Tyr	Phe	Gln	Ser	Ala	Gly					
			420					425					430							
aaa	atc	ggc	ttc	gag	aag	cct	gcc	agt	ggc	cta	gag	tac	gac	cag	ttc	1404				
Lys	Ile	Gly	Phe	Glu	Lys	Pro	Ala	Ser	Gly	Leu	Glu	Tyr	Asp	Gln	Phe					
		435					440					445								
ctc	agc	gac	ccg	gct	cac	cca	gtg	cct	ttc	acc	gaa	gct	acg	gct	acg	1452				
Leu	Ser	Asp	Pro	Ala	His	Pro	Val	Pro	Phe	Thr	Glu	Ala	Thr	Ala	Thr					
	450					455					460									
ggc	atg	acc	cgc	gag	tac	atg	acc	gac	gac	cag	cgc	ttc	gcc	agc	cgc	1500				
Gly	Met	Thr	Arg	Glu	Tyr	Met	Thr	Asp	Asp	Gln	Arg	Phe	Ala	Ser	Arg					
465					470				475						480					
cgc	ccc	gac	gtg	ctg	acc	tac	cag	acc	gaa	gcg	ctt	acc	gag	gac	atg	1548				
Arg	Pro	Asp	Val	Leu	Thr	Tyr	Gln	Thr	Glu	Ala	Leu	Thr	Glu	Asp	Met					
				485					490					495						
acg	ctg	gct	ggc	cct	atc	gag	gcg	ctg	ttg	cag	gta	gcc	acc	acc	ggc	1596				
Thr	Leu	Ala	Gly	Pro	Ile	Glu	Ala	Leu	Leu	Gln	Val	Ala	Thr	Thr	Gly					
			500					505					510							
acc	gat	gcc	gac	tgg	gta	gtg	aag	att	att	gat	gtg	tac	ccc	gac	gat	1644				
Thr	Asp	Ala	Asp	Trp	Val	Val	Lys	Ile	Ile	Asp	Val	Tyr	Pro	Asp	Asp					
		515					520					525								
acg	ccc	aac	aac	ccc	agc	acg	aac	ccc	gcc	gtg	aaa	ctg	ggc	ggc	tac	1692				
Thr	Pro	Asn	Asn	Pro	Ser	Thr	Asn	Pro	Ala	Val	Lys	Leu	Gly	Gly	Tyr					

530	535	540	
cag cag atg gtt cgc tcc gag gtg atg cgc ggt cgt ttc cgc aac agc			1740
Gln Gln Met Val Arg Ser Glu Val Met Arg Gly Arg Phe Arg Asn Ser			
545	550	555	560
ttc tcc aag ccc gaa gcc ttt gta ccg gaa cag gta acg gcc gtg ccc			1788
Phe Ser Lys Pro Glu Ala Phe Val Pro Glu Gln Val Thr Ala Val Pro			
	565	570	575
ttc acg gtg cag gac ctg tgc cac acc ttc cgg aaa gga cac cgc ctg			1836
Phe Thr Val Gln Asp Leu Cys His Thr Phe Arg Lys Gly His Arg Leu			
	580	585	590
atg gtg cag gtg caa agc agc tgg ttc ccg att gtt gac cgc aac ccg			1884
Met Val Gln Val Gln Ser Ser Trp Phe Pro Ile Val Asp Arg Asn Pro			
	595	600	605
cag acc ttc gta ccc aat att ttc gag gcc gat gag aag gat ttc cag			1932
Gln Thr Phe Val Pro Asn Ile Phe Glu Ala Asp Glu Lys Asp Phe Gln			
	610	615	620
gcc gcc acg cat cgg ctg tac cat tcg ccg gcg cat agc tcg cag ctc			1980
Ala Ala Thr His Arg Leu Tyr His Ser Pro Ala His Ser Ser Gln Leu			
	625	630	635
acg ttg cgc gtt ctg taggccactc taaacaggct cgg			2018
Thr Leu Arg Val Leu			
	645		

<210> 23
 <211> 645
 <212> PRT
 <213> Taxeobacter gelupurpurascens

<400> 23

Met	Pro	Tyr	Ser	Phe	Pro	Lys	Val	Ala	Ala	Leu	Ser	Gly	Leu	Leu	Val
1				5					10					15	
Ala	Gly	Leu	Ser	Gly	Ala	His	Ala	Gln	Thr	Pro	Val	Thr	Tyr	Pro	Leu
			20					25					30		
Ala	Ser	Glu	Ala	Glu	Lys	Ala	Gln	Leu	Ala	Val	Val	Leu	Ala	Asp	Thr
		35					40					45			
Ala	Tyr	Ile	Lys	Glu	Arg	Tyr	Thr	Lys	Thr	Glu	Tyr	Gln	Ile	Pro	Met
	50					55					60				

Arg 65	Asp	Gly	Val	Lys 70	Leu	Tyr	Thr	Ile	Val	Tyr 75	Ala	Pro	Asn	Asp	Ala 80
Asn	Lys	Val	Lys 85	Tyr	Pro	Ile	Leu	Leu	Asn 90	Arg	Thr	Pro	Tyr	Ala 95	Ile
Gly	Pro	Tyr	Gly 100	Pro	Gly	Lys	Tyr	Lys 105	Leu	Asn	Leu	Gly	Pro 110	Ser	Ser
Thr	Met	Met 115	His	Glu	Gly	Tyr	Ile 120	Phe	Ala	Tyr	Gln	Asp 125	Val	Arg	Gly
Arg	Tyr 130	Met	Ser	Glu	Gly	Glu 135	Phe	Val	Asp	Val	Arg 140	Pro	Glu	Lys	Asp
Met 145	His	Lys	Gly	Lys	Asn 150	Asp	Ile	Asp	Glu	Gly 155	Thr	Asp	Thr	Tyr	Asp 160
Thr	Ile	Glu	Trp	Leu 165	Leu	Lys	His	Gly	Pro 170	Lys	Asn	Asn	Gly	Arg 175	Val
Gly	Gln	Trp	Gly 180	Ile	Ser	Tyr	Pro	Gly 185	Tyr	Tyr	Thr	Ala	Thr 190	Gly	Leu
Leu	Ser	Arg 195	His	Lys	Ala	Leu	Lys 200	Ala	Ser	Ser	Pro	Gln 205	Ala	Pro	Ile
Ala	Asp 210	Trp	Phe	Trp	Asp	Asp 215	Phe	His	His	Asn	Gly 220	Ala	Phe	Phe	Leu
Pro 225	His	Ala	Phe	Asn	Phe 230	Leu	Ala	Ser	Phe	Gly 235	Leu	Ala	Arg	Pro	Gln 240
Pro	Thr	Pro	Thr	Gly 245	Asn	Pro	Gly	Phe	Lys 250	His	Gly	Thr	Pro	Asp 255	Gly
Tyr	Asp	Phe	Phe 260	Leu	Lys	Met	Gly	Pro 265	Leu	Lys	Asn	Ala	Asp 270	Ala	Asn

Tyr Tyr Lys Gly Lys Val Ala Phe Trp Asn Glu Met Ala Ser His Pro
 275 280 285

Asn Tyr Asp Glu Phe Trp Gln Ala Arg Asn Leu Arg Pro His Leu Lys
 290 295 300

Asn Leu Asn Lys Gly Thr Ala Val Leu Thr Val Gly Gly Phe Asn Asp
 305 310 315 320

Ala Glu Asp Leu Phe Gly Ala Leu Lys Thr Tyr Glu Ser Ile Glu Lys
 325 330 335

Gln Asn Pro Gly Met Arg Asn Gly Leu Val Met Gly Pro Trp Val His
 340 345 350

Gly Gly Trp Ala Arg Gly Thr Gly Glu Met Val Gly Asn Val Ala Tyr
 355 360 365

Gly Glu Ser Pro Ser Leu Tyr Tyr Gln Lys Gln Ile Glu Ala Pro Phe
 370 375 380

Phe Lys Ser Tyr Leu Lys Asp Gly Lys Pro Ala Ala Thr Pro Glu Ala
 385 390 395 400

Thr Ile Phe Glu Ser Gly Thr Asn Arg Trp Arg Ser Phe Glu Thr Trp
 405 410 415

Pro Pro Lys Glu Ala Lys Glu Arg Thr Leu Tyr Phe Gln Ser Ala Gly
 420 425 430

Lys Ile Gly Phe Glu Lys Pro Ala Ser Gly Leu Glu Tyr Asp Gln Phe
 435 440 445

Leu Ser Asp Pro Ala His Pro Val Pro Phe Thr Glu Ala Thr Ala Thr
 450 455 460

Gly Met Thr Arg Glu Tyr Met Thr Asp Asp Gln Arg Phe Ala Ser Arg
 465 470 475 480

Arg Pro Asp Val Leu Thr Tyr Gln Thr Glu Ala Leu Thr Glu Asp Met
485 490 495

Thr Leu Ala Gly Pro Ile Glu Ala Leu Leu Gln Val Ala Thr Thr Gly
500 505 510

Thr Asp Ala Asp Trp Val Val Lys Ile Ile Asp Val Tyr Pro Asp Asp
515 520 525

Thr Pro Asn Asn Pro Ser Thr Asn Pro Ala Val Lys Leu Gly Gly Tyr
530 535 540

Gln Gln Met Val Arg Ser Glu Val Met Arg Gly Arg Phe Arg Asn Ser
545 550 555 560

Phe Ser Lys Pro Glu Ala Phe Val Pro Glu Gln Val Thr Ala Val Pro
565 570 575

Phe Thr Val Gln Asp Leu Cys His Thr Phe Arg Lys Gly His Arg Leu
580 585 590

Met Val Gln Val Gln Ser Ser Trp Phe Pro Ile Val Asp Arg Asn Pro
595 600 605

Gln Thr Phe Val Pro Asn Ile Phe Glu Ala Asp Glu Lys Asp Phe Gln
610 615 620

Ala Ala Thr His Arg Leu Tyr His Ser Pro Ala His Ser Ser Gln Leu
625 630 635 640

Thr Leu Arg Val Leu
645

<210> 24
<211> 1931
<212> DNA
<213> *Cyclobacterium marinum*

<220>
<221> CDS
<222> (29)..(1888)

<223>

<400> 24

cccaaagcat taacaaaata atttagtc atg aaa cac tgt tac aaa ctt ctg	52
Met Lys His Cys Tyr Lys Leu Leu	
1 5	
gtc ttt tac aca tta ttt ttg atg acc aca aac tgg gct tta tca caa	100
Val Phe Tyr Thr Leu Phe Leu Met Thr Thr Asn Trp Ala Leu Ser Gln	
10 15 20	
gcc att aat gga tat gat aag gca gcc tat gac att cct atg cga gat	148
Ala Ile Asn Gly Tyr Asp Lys Ala Ala Tyr Asp Ile Pro Met Arg Asp	
25 30 35 40	
gga gtt cac ctt cac acc atc gtc tat agc ccc aaa gat tta tcg cag	196
Gly Val His Leu His Thr Ile Val Tyr Ser Pro Lys Asp Leu Ser Gln	
45 50 55	
ccc tat cct ata ttg atg caa agg aca cct tac agc gcc ggc cct tat	244
Pro Tyr Pro Ile Leu Met Gln Arg Thr Pro Tyr Ser Ala Gly Pro Tyr	
60 65 70	
ggg cct gga aat atg aaa aat aag ctt ggc cct tct cag ttt tta atg	292
Gly Pro Gly Asn Met Lys Asn Lys Leu Gly Pro Ser Gln Phe Leu Met	
75 80 85	
aac gat ggc tat ata ttt gtt tac cag gat gta aga ggg cgg tgg atg	340
Asn Asp Gly Tyr Ile Phe Val Tyr Gln Asp Val Arg Gly Arg Trp Met	
90 95 100	
tcg gaa gga tcc tat gac aac atg cgc cct acc cta tcc aaa tca gaa	388
Ser Glu Gly Ser Tyr Asp Asn Met Arg Pro Thr Leu Ser Lys Ser Glu	
105 110 115 120	
aga aat tcc aac caa ata gac gaa agc aca gac acc tat gat acc ata	436
Arg Asn Ser Asn Gln Ile Asp Glu Ser Thr Asp Thr Tyr Asp Thr Ile	
125 130 135	
gaa tgg ttg ctc gcc aat atc aaa aat cac aat gaa aaa gta ggc cta	484
Glu Trp Leu Leu Ala Asn Ile Lys Asn His Asn Glu Lys Val Gly Leu	
140 145 150	
tgg gga atc agc tat ccc gga ttt tat agt gct gca gcc ctt cct ttt	532
Trp Gly Ile Ser Tyr Pro Gly Phe Tyr Ser Ala Ala Leu Pro Phe	
155 160 165	
gcc cat cca aac ctg aaa gcc gtt tcc cct caa gca ccc ata ggg gat	580
Ala His Pro Asn Leu Lys Ala Val Ser Pro Gln Ala Pro Ile Gly Asp	
170 175 180	
ttt tac ttt gat gat ttt cat cat aac ggt gct tac tta tta agt tat	628

Phe 185	Tyr	Phe	Asp	Asp	Phe 190	His	His	Asn	Gly	Ala 195	Tyr	Leu	Leu	Ser	Tyr 200	
tgg	ttg	gcc	act	tct	gtt	ttc	ggc	tac	caa	aaa	gac	ggc	cct	aca	cag	676
Trp	Leu	Ala	Thr	Ser 205	Val	Phe	Gly	Tyr	Gln 210	Lys	Asp	Gly	Pro	Thr 215	Gln	
gaa	gca	tgg	tat	ggc	atg	gtg	aat	ccg	gaa	aca	aat	gac	ggc	tat	cag	724
Glu	Ala	Trp	Tyr 220	Gly	Met	Val	Asn	Pro 225	Glu	Thr	Asn	Asp	Gly	Tyr 230	Gln	
ttt	ttt	atg	gat	atg	ggg	cca	tta	aaa	aat	gcc	gat	aaa	tgg	tat	ggt	772
Phe	Phe	Met 235	Asp	Met	Gly	Pro	Leu 240	Lys	Asn	Ala	Asp	Lys 245	Trp	Tyr	Gly	
gaa	gac	aat	ttt	ttc	tgg	caa	caa	ctt	aaa	aac	aat	cct	gat	tac	aac	820
Glu	Asp 250	Asn	Phe	Phe	Trp	Gln 255	Gln	Leu	Lys	Asn	Asn 260	Pro	Asp	Tyr	Asn	
gct	ttc	tgg	caa	aag	aga	agt	att	att	cct	cac	tta	aaa	gaa	gtg	aag	868
Ala 265	Phe	Trp	Gln	Lys	Arg 270	Ser	Ile	Ile	Pro	His 275	Leu	Lys	Glu	Val	Lys 280	
cct	gca	gtt	tta	acc	gtt	ggg	ggc	tgg	ttt	gat	gca	gaa	gat	ctc	tat	916
Pro	Ala	Val	Leu	Thr 285	Val	Gly	Gly	Trp	Phe 290	Asp	Ala	Glu	Asp	Leu 295	Tyr	
gga	cca	ctt	aca	att	tat	aaa	acc	att	gaa	aaa	aat	aat	cct	gag	acc	964
Gly	Pro	Leu	Thr 300	Ile	Tyr	Lys	Thr	Ile 305	Glu	Lys	Asn	Asn	Pro 310	Glu	Thr	
tac	aat	acc	att	gtc	atg	ggc	cct	tgg	tcc	cac	gga	gat	tgg	tca	agg	1012
Tyr	Asn	Thr 315	Ile	Val	Met	Gly	Pro 320	Trp	Ser	His	Gly	Asp 325	Trp	Ser	Arg	
gaa	cct	gga	tca	cag	gtc	att	tca	aat	att	tat	ttt	ggt	gat	tct	atc	1060
Glu	Pro 330	Gly	Ser	Gln	Val	Ile 335	Ser	Asn	Ile	Tyr	Phe 340	Gly	Asp	Ser	Ile	
tcc	aca	tgg	tat	caa	aaa	aat	ata	gaa	cgt	gtt	ttt	ttc	aat	cat	ttt	1108
Ser 345	Thr	Trp	Tyr	Gln	Lys 350	Asn	Ile	Glu	Arg	Val 355	Phe	Phe	Asn	His	Phe 360	
cta	aaa	gaa	tcc	gaa	aat	agc	aat	cct	gcc	ctt	cct	gaa	gcc	tac	atg	1156
Leu	Lys	Glu	Ser	Glu 365	Asn	Ser	Asn	Pro	Ala 370	Leu	Pro	Glu	Ala	Tyr 375	Met	
ttt	gat	acc	gga	aaa	cat	aaa	tgg	gaa	aaa	ttt	gac	gat	tgg	cct	cct	1204
Phe	Asp	Thr 380	Gly	Lys	His	Lys	Trp	Glu 385	Lys	Phe	Asp	Asp	Trp 390	Pro	Pro	
aaa	gaa	agc	caa	tgg	aaa	agc	ttt	tac	ttt	caa	gag	aaa	gga	gag	tta	1252

Lys	Glu	Ser	Gln	Trp	Lys	Ser	Phe	Tyr	Phe	Gln	Glu	Lys	Gly	Glu	Leu	
		395					400					405				
act	gag	gta	aca	cct	gag	gga	aat	agg	ttt	act	acc	tat	gtc	tca	gac	1300
Thr	Glu	Val	Thr	Pro	Glu	Gly	Asn	Arg	Phe	Thr	Thr	Tyr	Val	Ser	Asp	
	410					415					420					
ccc	tct	aat	cct	gtc	ccc	tat	agt	caa	gat	att	aaa	cta	aac	ttc	act	1348
Pro	Ser	Asn	Pro	Val	Pro	Tyr	Ser	Gln	Asp	Ile	Lys	Leu	Asn	Phe	Thr	
425					430					435					440	
ccg	aga	aaa	tac	atg	gcc	gat	gac	cag	cga	ttt	gca	gcc	aga	aga	ccg	1396
Pro	Arg	Lys	Tyr	Met	Ala	Asp	Asp	Gln	Arg	Phe	Ala	Ala	Arg	Arg	Pro	
				445					450					455		
gac	gta	ctg	acc	ttt	acg	agc	gaa	gta	tta	agt	caa	gac	atg	acg	ctt	1444
Asp	Val	Leu	Thr	Phe	Thr	Ser	Glu	Val	Leu	Ser	Gln	Asp	Met	Thr	Leu	
			460					465					470			
gcg	ggg	gaa	gtc	atg	gca	aac	tta	aaa	gtt	gcc	act	tca	caa	act	gat	1492
Ala	Gly	Glu	Val	Met	Ala	Asn	Leu	Lys	Val	Ala	Thr	Ser	Gln	Thr	Asp	
		475					480					485				
gct	gat	tgg	gta	gtt	aaa	atc	atc	gat	ata	ttt	ccc	gga	gat	cag	cca	1540
Ala	Asp	Trp	Val	Val	Lys	Ile	Ile	Asp	Ile	Phe	Pro	Gly	Asp	Gln	Pro	
	490					495					500					
aat	cat	gcc	tat	gtt	tta	gat	ggg	gtg	gac	atg	ggc	aat	tac	cac	cta	1588
Asn	His	Ala	Tyr	Val	Leu	Asp	Gly	Val	Asp	Met	Gly	Asn	Tyr	His	Leu	
505					510					515					520	
atg	gtt	cgt	tca	gag	gta	att	aga	ggg	agg	tat	aga	gaa	agt	ttt	gag	1636
Met	Val	Arg	Ser	Glu	Val	Ile	Arg	Gly	Arg	Tyr	Arg	Glu	Ser	Phe	Glu	
				525					530					535		
ttt	cct	aaa	ccc	ttt	gtt	cct	gat	caa	atc	act	gct	gtt	gat	ttc	agg	1684
Phe	Pro	Lys	Pro	Phe	Val	Pro	Asp	Gln	Ile	Thr	Ala	Val	Asp	Phe	Arg	
			540					545					550			
tta	caa	gat	ctt	ttc	cat	act	ttc	aaa	aag	ggg	cat	aaa	att	caa	ata	1732
Leu	Gln	Asp	Leu	Phe	His	Thr	Phe	Lys	Lys	Gly	His	Lys	Ile	Gln	Ile	
		555					560					565				
caa	ata	caa	agt	act	tgg	ttt	ccc	cta	att	gat	cga	aat	ccc	caa	aaa	1780
Gln	Ile	Gln	Ser	Thr	Trp	Phe	Pro	Leu	Ile	Asp	Arg	Asn	Pro	Gln	Lys	
	570					575					580					
tat	gta	caa	aac	ata	ttt	gaa	gct	gag	gaa	gcc	gat	ttt	gtc	aaa	gcc	1828
Tyr	Val	Gln	Asn	Ile	Phe	Glu	Ala	Glu	Glu	Ala	Asp	Phe	Val	Lys	Ala	
585					590					595					600	
acc	cat	agg	gtt	ttt	cat	aca	gaa	aag	ttt	gcc	agc	aaa	att	gaa	gta	1876

Thr His Arg Val Phe His Thr Glu Lys Phe Ala Ser Lys Ile Glu Val
605 610 615

atg gtt ctt cct tagaattaga atggtttaaa attactatatt gtagcagaag ata 1931
Met Val Leu Pro
620

<210> 25
<211> 620
<212> PRT
<213> Cyclobacterium marinum

<400> 25

Met Lys His Cys Tyr Lys Leu Leu Val Phe Tyr Thr Leu Phe Leu Met
1 5 10 15

Thr Thr Asn Trp Ala Leu Ser Gln Ala Ile Asn Gly Tyr Asp Lys Ala
20 25 30

Ala Tyr Asp Ile Pro Met Arg Asp Gly Val His Leu His Thr Ile Val
35 40 45

Tyr Ser Pro Lys Asp Leu Ser Gln Pro Tyr Pro Ile Leu Met Gln Arg
50 55 60

Thr Pro Tyr Ser Ala Gly Pro Tyr Gly Pro Gly Asn Met Lys Asn Lys
65 70 75 80

Leu Gly Pro Ser Gln Phe Leu Met Asn Asp Gly Tyr Ile Phe Val Tyr
85 90 95

Gln Asp Val Arg Gly Arg Trp Met Ser Glu Gly Ser Tyr Asp Asn Met
100 105 110

Arg Pro Thr Leu Ser Lys Ser Glu Arg Asn Ser Asn Gln Ile Asp Glu
115 120 125

Ser Thr Asp Thr Tyr Asp Thr Ile Glu Trp Leu Leu Ala Asn Ile Lys
130 135 140

Asn His Asn Glu Lys Val Gly Leu Trp Gly Ile Ser Tyr Pro Gly Phe

145		150		155		160									
Tyr	Ser	Ala	Ala	Ala	Leu	Pro	Phe	Ala	His	Pro	Asn	Leu	Lys	Ala	Val
				165					170					175	
Ser	Pro	Gln	Ala	Pro	Ile	Gly	Asp	Phe	Tyr	Phe	Asp	Asp	Phe	His	His
			180					185					190		
Asn	Gly	Ala	Tyr	Leu	Leu	Ser	Tyr	Trp	Leu	Ala	Thr	Ser	Val	Phe	Gly
		195					200					205			
Tyr	Gln	Lys	Asp	Gly	Pro	Thr	Gln	Glu	Ala	Trp	Tyr	Gly	Met	Val	Asn
	210					215					220				
Pro	Glu	Thr	Asn	Asp	Gly	Tyr	Gln	Phe	Phe	Met	Asp	Met	Gly	Pro	Leu
225					230					235					240
Lys	Asn	Ala	Asp	Lys	Trp	Tyr	Gly	Glu	Asp	Asn	Phe	Phe	Trp	Gln	Gln
				245					250					255	
Leu	Lys	Asn	Asn	Pro	Asp	Tyr	Asn	Ala	Phe	Trp	Gln	Lys	Arg	Ser	Ile
			260					265					270		
Ile	Pro	His	Leu	Lys	Glu	Val	Lys	Pro	Ala	Val	Leu	Thr	Val	Gly	Gly
		275					280					285			
Trp	Phe	Asp	Ala	Glu	Asp	Leu	Tyr	Gly	Pro	Leu	Thr	Ile	Tyr	Lys	Thr
	290					295					300				
Ile	Glu	Lys	Asn	Asn	Pro	Glu	Thr	Tyr	Asn	Thr	Ile	Val	Met	Gly	Pro
305					310					315					320
Trp	Ser	His	Gly	Asp	Trp	Ser	Arg	Glu	Pro	Gly	Ser	Gln	Val	Ile	Ser
				325					330					335	
Asn	Ile	Tyr	Phe	Gly	Asp	Ser	Ile	Ser	Thr	Trp	Tyr	Gln	Lys	Asn	Ile
			340					345					350		
Glu	Arg	Val	Phe	Phe	Asn	His	Phe	Leu	Lys	Glu	Ser	Glu	Asn	Ser	Asn

355

360

365

Pro Ala Leu Pro Glu Ala Tyr Met Phe Asp Thr Gly Lys His Lys Trp
 370 375 380

Glu Lys Phe Asp Asp Trp Pro Pro Lys Glu Ser Gln Trp Lys Ser Phe
 385 390 395 400

Tyr Phe Gln Glu Lys Gly Glu Leu Thr Glu Val Thr Pro Glu Gly Asn
 405 410 415

Arg Phe Thr Thr Tyr Val Ser Asp Pro Ser Asn Pro Val Pro Tyr Ser
 420 425 430

Gln Asp Ile Lys Leu Asn Phe Thr Pro Arg Lys Tyr Met Ala Asp Asp
 435 440 445

Gln Arg Phe Ala Ala Arg Arg Pro Asp Val Leu Thr Phe Thr Ser Glu
 450 455 460

Val Leu Ser Gln Asp Met Thr Leu Ala Gly Glu Val Met Ala Asn Leu
 465 470 475 480

Lys Val Ala Thr Ser Gln Thr Asp Ala Asp Trp Val Val Lys Ile Ile
 485 490 495

Asp Ile Phe Pro Gly Asp Gln Pro Asn His Ala Tyr Val Leu Asp Gly
 500 505 510

Val Asp Met Gly Asn Tyr His Leu Met Val Arg Ser Glu Val Ile Arg
 515 520 525

Gly Arg Tyr Arg Glu Ser Phe Glu Phe Pro Lys Pro Phe Val Pro Asp
 530 535 540

Gln Ile Thr Ala Val Asp Phe Arg Leu Gln Asp Leu Phe His Thr Phe
 545 550 555 560

Lys Lys Gly His Lys Ile Gln Ile Gln Ile Gln Ser Thr Trp Phe Pro

565

570

575

Leu Ile Asp Arg Asn Pro Gln Lys Tyr Val Gln Asn Ile Phe Glu Ala
 580 585 590

Glu Glu Ala Asp Phe Val Lys Ala Thr His Arg Val Phe His Thr Glu
 595 600 605

Lys Phe Ala Ser Lys Ile Glu Val Met Val Leu Pro
 610 615 620

<210> 26

<211> 2036

<212> DNA

<213> *Psycloserpens burtonensis*

<220>

<221> CDS

<222> (61)..(1992)

<223>

<400> 26

catatttcgta	aaatagctat	aagttttttgt	aaatttagtc	aatcaaaatt	ttaaattgtaa	60
atg aag act ctt ttt aaa ttg ttg ctc cta ttt gta ttt gtt cta acg	108					
Met Lys Thr Leu Phe Lys Leu Leu Leu Leu Phe Val Phe Val Leu Thr						
1 5 10 15						
tct tgt aat aag gcc aac aaa gac gct act gaa att gtg aaa acc gaa	156					
Ser Cys Asn Lys Ala Asn Lys Asp Ala Thr Glu Ile Val Lys Thr Glu						
20 25 30						
gta gaa gat act tac gtt aaa gat aat tat aac aaa caa gag gtg act	204					
Val Glu Asp Thr Tyr Val Lys Asp Asn Tyr Asn Lys Gln Glu Val Thr						
35 40 45						
att gaa atg cgc gat ggt ata aaa ctt cac acg acc att tat tca cca	252					
Ile Glu Met Arg Asp Gly Ile Lys Leu His Thr Thr Ile Tyr Ser Pro						
50 55 60						
aaa gat gaa agt cag acc tat cct att tta atg atg aga aca cca tat	300					
Lys Asp Glu Ser Gln Thr Tyr Pro Ile Leu Met Met Arg Thr Pro Tyr						
65 70 75 80						
agt tct caa cct tat ggt gac aat gag ttt aag acg aaa att ggt cct	348					
Ser Ser Gln Pro Tyr Gly Asp Asn Glu Phe Lys Thr Lys Ile Gly Pro						
85 90 95						

aat gtt cat tta atg aaa gaa ggg aat att gtt gtg tat caa gat gta	396
Asn Val His Leu Met Lys Glu Gly Asn Ile Val Val Tyr Gln Asp Val	
100 105 110	
cga ggt cgt tgg atg agt gaa ggt gtc tat gat aat atg cgt gct tat	444
Arg Gly Arg Trp Met Ser Glu Gly Val Tyr Asp Asn Met Arg Ala Tyr	
115 120 125	
atc cca aat aaa aca gag gat tct caa att gat gag gca tca gac act	492
Ile Pro Asn Lys Thr Glu Asp Ser Gln Ile Asp Glu Ala Ser Asp Thr	
130 135 140	
tat gac acg att gac tgg ctg gta aat aac gta gaa aat aat aac ggg	540
Tyr Asp Thr Ile Asp Trp Leu Val Asn Asn Val Glu Asn Asn Asn Gly	
145 150 155 160	
aat gtt ggt act tgg gga att tca tat cct ggt ttt tat gct aca tat	588
Asn Val Gly Thr Trp Gly Ile Ser Tyr Pro Gly Phe Tyr Ala Thr Tyr	
165 170 175	
tct act ata gac gca cac cca gct tta aaa gca gca tcg cct caa gcg	636
Ser Thr Ile Asp Ala His Pro Ala Leu Lys Ala Ala Ser Pro Gln Ala	
180 185 190	
tgt att gga gat ttc ttt ttt gac gat ttt cat cat aat ggt gct ttt	684
Cys Ile Gly Asp Phe Phe Phe Asp Asp Phe His His Asn Gly Ala Phe	
195 200 205	
tta tta agt tat ttt aga gca gtg tct tta ttt ggt acg aca aaa gat	732
Leu Leu Ser Tyr Phe Arg Ala Val Ser Leu Phe Gly Thr Thr Lys Asp	
210 215 220	
aaa cct aca gat tct gct tgg tat aag ttt cca gaa atg aaa aca caa	780
Lys Pro Thr Asp Ser Ala Trp Tyr Lys Phe Pro Glu Met Lys Thr Gln	
225 230 235 240	
gat caa tat caa ttt ttt ctt gat gct gga cct tta agt aat ttg aac	828
Asp Gln Tyr Gln Phe Phe Leu Asp Ala Gly Pro Leu Ser Asn Leu Asn	
245 250 255	
aag tat ttc caa tat gac aca cca gac gac aca tct gta tcc aag tct	876
Lys Tyr Phe Gln Tyr Asp Thr Pro Asp Asp Thr Ser Val Ser Lys Ser	
260 265 270	
gat agg ata gat gat gtg ttt tgg aaa gaa att gta gag cat cca aac	924
Asp Arg Ile Asp Asp Val Phe Trp Lys Glu Ile Val Glu His Pro Asn	
275 280 285	
tac gat acg ata tgg aaa tct aaa ggt tta att caa aac cta aaa gat	972
Tyr Asp Thr Ile Trp Lys Ser Lys Gly Leu Ile Gln Asn Leu Lys Asp	
290 295 300	

att aag cca agt gta gcg aca atg att gtg gga ggg tta ttt gat gcc Ile Lys Pro Ser Val Ala Thr Met Ile Val Gly Gly Leu Phe Asp Ala 305 310 315 320	1020
gaa gat tta tat ggg cca ttt gaa act tat aaa acg ata gaa aaa cat Glu Asp Leu Tyr Gly Pro Phe Glu Thr Tyr Lys Thr Ile Glu Lys His 325 330 335	1068
aat cct gat aat tat aat att atg gtt ttt ggg cct tgg gat cat ggt Asn Pro Asp Asn Tyr Asn Ile Met Val Phe Gly Pro Trp Asp His Gly 340 345 350	1116
cgt tgg gct agg agt gac gtt aaa aat tat gtt gga aat tat ttc ttc Arg Trp Ala Arg Ser Asp Val Lys Asn Tyr Val Gly Asn Tyr Phe Phe 355 360 365	1164
gga gat tct ata tct cta aaa ttt caa cgt gat gtt gaa acg aag ttt Gly Asp Ser Ile Ser Leu Lys Phe Gln Arg Asp Val Glu Thr Lys Phe 370 375 380	1212
ttt aat cat ttt tta aaa gga aaa ggc gac aag aac tca ggg tta cca Phe Asn His Phe Leu Lys Gly Lys Gly Asp Lys Asn Ser Gly Leu Pro 385 390 395 400	1260
gaa gca tat gta ttt gat tct ggt aaa aag gaa tgg agt agc ttt gac Glu Ala Tyr Val Phe Asp Ser Gly Lys Lys Glu Trp Ser Ser Phe Asp 405 410 415	1308
agc tgg cct cca aag caa gca gaa aaa caa gcc atg tat ctt aat gcc Ser Trp Pro Pro Lys Gln Ala Glu Lys Gln Ala Met Tyr Leu Asn Ala 420 425 430	1356
aac caa gag cta tca gat tca aaa aaa gga aat act agt gag aca ttt Asn Gln Glu Leu Ser Asp Ser Lys Lys Gly Asn Thr Ser Glu Thr Phe 435 440 445	1404
gtt agt gat tta aaa cgc cct gta cct tat tcc gaa gat att aaa aca Val Ser Asp Leu Lys Arg Pro Val Pro Tyr Ser Glu Asp Ile Lys Thr 450 455 460	1452
gtt ttc aca cca cga aaa tac atg aca gac gat cag cgt ttt gca gca Val Phe Thr Pro Arg Lys Tyr Met Thr Asp Asp Gln Arg Phe Ala Ala 465 470 475 480	1500
cga cgt cct gat gtt ctt ata ttt gag acc gat att ctt gag gaa gat Arg Arg Pro Asp Val Leu Ile Phe Glu Thr Asp Ile Leu Glu Glu Asp 485 490 495	1548
ata acc tta gct ggt gat att tta gcg cag ctt aat gtg tca act aca Ile Thr Leu Ala Gly Asp Ile Leu Ala Gln Leu Asn Val Ser Thr Thr 500 505 510	1596

ggg aca gat gca gat tgg att gtc aaa ata gta gat gtt cat cca gca	1644
Gly Thr Asp Ala Asp Trp Ile Val Lys Ile Val Asp Val His Pro Ala	
515 520 525	
gat gct gag gag caa aaa gaa ggt atg caa gac cat tta tca atg agt	1692
Asp Ala Glu Glu Gln Lys Glu Gly Met Gln Asp His Leu Ser Met Ser	
530 535 540	
aat tat cat ttg atg gtg agg agt gaa gtg atg cgc ggt cgt ttt aga	1740
Asn Tyr His Leu Met Val Arg Ser Glu Val Met Arg Gly Arg Phe Arg	
545 550 555 560	
aat agt ttt gaa aac cca gag cca ttt gtg cca aac caa cca aca gat	1788
Asn Ser Phe Glu Asn Pro Glu Pro Phe Val Pro Asn Gln Pro Thr Asp	
565 570 575	
gtc aat atc aag tta caa gat gta cat cat aca ttt aaa aaa ggt cac	1836
Val Asn Ile Lys Leu Gln Asp Val His His Thr Phe Lys Lys Gly His	
580 585 590	
aaa tta caa gtg caa gtt cag agt acg tgg ttt cca ctt att gat ttg	1884
Lys Leu Gln Val Gln Val Gln Ser Thr Trp Phe Pro Leu Ile Asp Leu	
595 600 605	
aac ccg caa aca ttt gtg cct aat att tat aaa gca aaa gaa agc gat	1932
Asn Pro Gln Thr Phe Val Pro Asn Ile Tyr Lys Ala Lys Glu Ser Asp	
610 615 620	
ttt aaa acc caa aca cat tcg gtt ttt aac gat tct aaa att gag ttt	1980
Phe Lys Thr Gln Thr His Ser Val Phe Asn Asp Ser Lys Ile Glu Phe	
625 630 635 640	
acg gtt ttg aaa taagagtaga tgactaaatt tgccaaggta gatttagtct tttt	2036
Thr Val Leu Lys	

<210> 27
 <211> 644
 <212> PRT
 <213> *Psycloserpens burtonensis*

<400> 27

Met Lys Thr Leu Phe Lys Leu Leu Leu Leu Phe Val Phe Val Leu Thr
1 5 10 15

Ser Cys Asn Lys Ala Asn Lys Asp Ala Thr Glu Ile Val Lys Thr Glu
20 25 30

Val	Glu	Asp	Thr	Tyr	Val	Lys	Asp	Asn	Tyr	Asn	Lys	Gln	Glu	Val	Thr		
		35					40					45					
Ile	Glu	Met	Arg	Asp	Gly	Ile	Lys	Leu	His	Thr	Thr	Ile	Tyr	Ser	Pro		
	50					55					60						
Lys	Asp	Glu	Ser	Gln	Thr	Tyr	Pro	Ile	Leu	Met	Met	Arg	Thr	Pro	Tyr		
65					70					75					80		
Ser	Ser	Gln	Pro	Tyr	Gly	Asp	Asn	Glu	Phe	Lys	Thr	Lys	Ile	Gly	Pro		
				85					90					95			
Asn	Val	His	Leu	Met	Lys	Glu	Gly	Asn	Ile	Val	Val	Tyr	Gln	Asp	Val		
			100					105					110				
Arg	Gly	Arg	Trp	Met	Ser	Glu	Gly	Val	Tyr	Asp	Asn	Met	Arg	Ala	Tyr		
		115					120					125					
Ile	Pro	Asn	Lys	Thr	Glu	Asp	Ser	Gln	Ile	Asp	Glu	Ala	Ser	Asp	Thr		
	130					135					140						
Tyr	Asp	Thr	Ile	Asp	Trp	Leu	Val	Asn	Asn	Val	Glu	Asn	Asn	Asn	Gly		
145					150					155					160		
Asn	Val	Gly	Thr	Trp	Gly	Ile	Ser	Tyr	Pro	Gly	Phe	Tyr	Ala	Thr	Tyr		
				165					170					175			
Ser	Thr	Ile	Asp	Ala	His	Pro	Ala	Leu	Lys	Ala	Ala	Ser	Pro	Gln	Ala		
			180					185					190				
Cys	Ile	Gly	Asp	Phe	Phe	Phe	Asp	Asp	Phe	His	His	Asn	Gly	Ala	Phe		
		195					200					205					
Leu	Leu	Ser	Tyr	Phe	Arg	Ala	Val	Ser	Leu	Phe	Gly	Thr	Thr	Lys	Asp		
	210					215					220						
Lys	Pro	Thr	Asp	Ser	Ala	Trp	Tyr	Lys	Phe	Pro	Glu	Met	Lys	Thr	Gln		
225					230					235					240		

Asp Gln Tyr Gln Phe Phe Leu Asp Ala Gly Pro Leu Ser Asn Leu Asn
 245 250 255

Lys Tyr Phe Gln Tyr Asp Thr Pro Asp Asp Thr Ser Val Ser Lys Ser
 260 265 270

Asp Arg Ile Asp Asp Val Phe Trp Lys Glu Ile Val Glu His Pro Asn
 275 280 285

Tyr Asp Thr Ile Trp Lys Ser Lys Gly Leu Ile Gln Asn Leu Lys Asp
 290 295 300

Ile Lys Pro Ser Val Ala Thr Met Ile Val Gly Gly Leu Phe Asp Ala
 305 310 315 320

Glu Asp Leu Tyr Gly Pro Phe Glu Thr Tyr Lys Thr Ile Glu Lys His
 325 330 335

Asn Pro Asp Asn Tyr Asn Ile Met Val Phe Gly Pro Trp Asp His Gly
 340 345 350

Arg Trp Ala Arg Ser Asp Val Lys Asn Tyr Val Gly Asn Tyr Phe Phe
 355 360 365

Gly Asp Ser Ile Ser Leu Lys Phe Gln Arg Asp Val Glu Thr Lys Phe
 370 375 380

Phe Asn His Phe Leu Lys Gly Lys Gly Asp Lys Asn Ser Gly Leu Pro
 385 390 395 400

Glu Ala Tyr Val Phe Asp Ser Gly Lys Lys Glu Trp Ser Ser Phe Asp
 405 410 415

Ser Trp Pro Pro Lys Gln Ala Glu Lys Gln Ala Met Tyr Leu Asn Ala
 420 425 430

Asn Gln Glu Leu Ser Asp Ser Lys Lys Gly Asn Thr Ser Glu Thr Phe
 435 440 445

Val	Ser	Asp	Leu	Lys	Arg	Pro	Val	Pro	Tyr	Ser	Glu	Asp	Ile	Lys	Thr
450						455					460				
Val	Phe	Thr	Pro	Arg	Lys	Tyr	Met	Thr	Asp	Asp	Gln	Arg	Phe	Ala	Ala
465					470					475					480
Arg	Arg	Pro	Asp	Val	Leu	Ile	Phe	Glu	Thr	Asp	Ile	Leu	Glu	Glu	Asp
				485					490					495	
Ile	Thr	Leu	Ala	Gly	Asp	Ile	Leu	Ala	Gln	Leu	Asn	Val	Ser	Thr	Thr
			500					505					510		
Gly	Thr	Asp	Ala	Asp	Trp	Ile	Val	Lys	Ile	Val	Asp	Val	His	Pro	Ala
		515					520					525			
Asp	Ala	Glu	Glu	Gln	Lys	Glu	Gly	Met	Gln	Asp	His	Leu	Ser	Met	Ser
	530					535					540				
Asn	Tyr	His	Leu	Met	Val	Arg	Ser	Glu	Val	Met	Arg	Gly	Arg	Phe	Arg
545					550					555					560
Asn	Ser	Phe	Glu	Asn	Pro	Glu	Pro	Phe	Val	Pro	Asn	Gln	Pro	Thr	Asp
				565					570					575	
Val	Asn	Ile	Lys	Leu	Gln	Asp	Val	His	His	Thr	Phe	Lys	Lys	Gly	His
			580					585					590		
Lys	Leu	Gln	Val	Gln	Val	Gln	Ser	Thr	Trp	Phe	Pro	Leu	Ile	Asp	Leu
		595					600					605			
Asn	Pro	Gln	Thr	Phe	Val	Pro	Asn	Ile	Tyr	Lys	Ala	Lys	Glu	Ser	Asp
	610					615					620				
Phe	Lys	Thr	Gln	Thr	His	Ser	Val	Phe	Asn	Asp	Ser	Lys	Ile	Glu	Phe
625					630					635					640
Thr	Val	Leu	Lys												